

FIG. 1

-54	AGCTGCGGCGCGGTCTGCCAGCCAGACCCCTTTGGAGAAGACCCCACTCCCTGTC
1	ATGGGGGCGCGCTGCACCTGCACCCCTTTCTCTCTCTGGTGAGGTGACAGCGCTGGCT 60
	<u>M G P R C T L H P L S L L V Q V T A L A</u>
61	GCGACTCTGGCCAGGGCAGGCTGCCCTGCCCTTCTGCGCTGTGAGCTCCAGCCCCACGGC 120
	<u>A T L A Q G R L P A F L P C E L Q P H G</u>
121	CTGGTGAACTGCAACTGGCTCTTCTGAAGTCCGTGCCCACTTCTGCGCGCAGCGCC 180
	L V N C N W L F L K S V P H F S A A A P
181	CGGGCCAAAGTCACAGCCTCTCCTTACTCTCCAAACCGCATCCACCTTGCAAGACTCT 240
	R A N V T S L S L L S N R I H H L H D S
241	GACTTCGTCCACTGTCCAGCTACGAACCTCTCAACCTCAAGTGGAACTGCCCGCGGCT 300
	D F V H L S S L R T L N L K W N C P P A
301	GCGCTCAGCCCATGCACCTTCCCTGCCACATGACCATCGAGCCCAACACCTTCTGCGC 360
	G L S P M H F P C H M T I E P N T F L A
361	GTGCCCAACCTGGAGGAGCTGAACCTGAGCTACAACAGCATCAGCAACGTGCGCTGCCCTG 420
	V P T L E E L N L S Y N S I T T V P A L
421	CCGACTCCCTGTGTCCCTGTGCTGAGCGCACCAACATCCTGGTGCTAGACCCCAAC 480
	P D S L V S L S L S R T N I L V L D P T
481	CACTCTACTGGCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAG 540
	H L T G L H A L R Y L Y M D G N C Y Y K
541	AACCCCTGCCAGGGGGCGCTGGAGGTGGTGCGGGGTGCCCTCTCGCGCTGGGCAACCTC 600
	N P C Q G A L E V V P G A L L G L G N L
601	ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCGCGACCTGCCCGCCAGC 660
	T H L S L K Y N N L T E V P R S L P P S
661	CTGAGACCTGCTGTGTGCTACAAACACATTGTCAACCTGACGCTGAGCACTGGCC 720
	L E T L L L S Y N H I V T L T P E D L A
721	AATCTGACTGCCCTGCGGTGCTTGATGTGGGGGGAACTGCGCGCGCTGTGACCATGCC 780
	N L T A L R V L D V G G N C R
	<u>(SEQ ID NO:1 1-834)</u>
	<u>(SEQ ID NO:2 1-260)</u>

FIG. 2

781 CGCAACCCCTGCAGGGAGTGCACAAAGGACCAACCCCAAGCTGCACCTCTGACACCTTCAGC 840
 R N P C R E C P K D H P K L H S D T F S
 841 CACCTGAGCCGCTCGAAGGCTGGTGTGAAAGACAGTTCTCTCTACAACTGGAGGCC 900
 H L S R L E G L V L K D S S L Y N L D A
 901 AGTGGTTCGAGGGCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACITCCTCTAC 960
 R W F R G L D R L Q V L D L S E N F L Y
 961 GACTGCATCAACCAAGACACGGCTTCCAGGGCTGGCCGACTGCGCAAGCTCAACCTG 1020
 D C I T K T T A F Q G L A R L R K L N L
 1021 TCCTTCAATTACCAAGAAGGTGTCTTTGCCCACTGCACCTGGCAACCTCCTTTGGG 1080
 S F N Y H K K V S F A H L H L A P S F G
 1081 CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCCGCTCGCTCAGTGAG 1140
 H L R S L K E L D M H G I F F R S L S E
 1141 ACCACGCTCCAACTCTGGTCCAAGTGCCTATGCTCCAGACCTGGCGCTGCAGATGAAC 1200
 T T L Q P L V Q L P M L Q T L R L Q M N
 1201 TTCATTAAACAGGCCCACTCAGCATCTTTGGGGCTTCCTCGGCTGCTGTGAAGTGGAC 1260
 F I N Q A Q L S I F G A F P G L L Y V D
 1261 CTATCGGACAAACGATCAGCGGAGCTGCAAGGCCAGTGGCATTACTAGCGAGGTGGAT 1320
 L S D N R I S G A A R P V A I T R E V D
 1321 GGTAGGAGAGGGTCTGGCTGCTTCCAGGAACCTGCTCCAGCTGCACTGGACACTCTC 1380
 G R E R V W L P S R N L A P R P L D T L
 1381 CGCTCAGAGGACTTCATGCCAACTGCAAGGCTTCAGCTTCACCTTGGAACTGTCTCGG 1440
 R S E D F M P N C K A F S F T L D L S R
 1441 AACAACTGGTGACAATCCAGTCGGAGATGTTTGCTCGCTCTCAGCGCTGAGTGGCTG 1500
 N N L V T I Q S E M F A R L S R L E C L
 1501 CGTCTGAGCCACAACAGCATCTCCAGGCGGCTCAATGGCTCTCAGTTTGTGGCGCTGACC 1560
 R L S H N S I S Q A V N G S

Amended

(SEQ ID NO:1 835-1614)

O F V P L T

(SEQ ID NO:2 261-520)

FIG. 3

1561 AGCCTGCGGGTGTCTGGACCTGTCCACACAACAGCTGGAOCTGTATCAGGGGCGCTCGTTC 1620
 S L R V L D L S H N K L D L Y H G R S F
 1621 ACGGAGCTGCCCGCGCTGGAAGCACTGGAOCTCAGCTACAACAGCCAGCCCTTTACCATG 1680
 T E L P R L E A L D L S Y N S Q P F T M
 1681 CAGGGTGTGGGCGACAACCTCAGCTTCGTGGCCAGCTGCCGCCCTGGCTACCTCAGC 1740
 Q G V G H N L S F V A Q L P A L R Y L S
 1741 CTGGCGACAATGACATCCATAGCCGAGTGTCCAGCAGCTCTGTAGCCCTCAGCTGTGC 1800
 L A H N D I H S R V S Q Q L C S A S L C
 1801 GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860
 A L D F S G N D L S R M W A E G D L Y L
 1861 CGCTTCTTCCAAGGCTAAGAAGCTTAGTCTGGCTGGAOCTGTCCAGAACCACTGCAC 1920
 R F F Q G L R S L V W L D L S Q N H L H
 1921 ACCCTCTGCCAGTGGCCCTGGACAACCTCCCCAAAAGCTGAAGCATCTGCATCTCCGT 1980
 T L L P R A L D N L P K S L K H L H L R
 1981 GACAATAACCTGGCCTTCTTCAACTGGAGCAGCTGACCTCTGCCCAAGCTGAAACC 2040
 D N N L A F F N W S S L T L L P K L E T
 2041 CTGGACTTGGCTGGAAACCACTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCAOC 2100
 L D L A G N Q L K A L S N G S L P S G T
 2101 CAGCTGCGGAGGCTGGAOCTCAGTGGCAACAGCATCGGCTTTGTGAACCTGGCTTCTTT 2160
 Q L R R L D L S G N S I G F V N P G F F
 2161 GCCCTGCCAAGCAGTTAGAAGAGCTCAACCTCAGGCCAATGCCCTCAAGACAGTGGAG 2220
 A L A K Q L E E L N L S A N A L K T V E
 2221 CCCTCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCTAGACGTGAGGCCAACCT 2280
 P S W F G S M V G N L K V L D V S A N P
 2281 CTGCACCTGCCCTGTGGGGGACCTTGTGGGCTTCTGCTGGAGGTACAGGCTGCCGTG 2340
 L H C A C G A T F V G F L L E V Q A A V

(SEQ ID NO:1 1615-2394)

Amended

(SEQ ID NO:2 521-780)

FIG. 4

2341 CCTGGGCTGCCCAGCCGGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC 2400
 P G L P S R V K C G S P G Q L Q G H S I
 2401 TTITGGCAAGAACTGGGCTCTGGCTGGATGAGACCTCTGGTGAAGTGTITGGCATC 2460
 F A Q D L R L C L D E T L S W N C F G I
 2461 TCGCTGCTGGCCATGGCCCTGGGCTGGTTGTGGCCATGCTGCACCACCTCTGGGGCTGG 2520
 S L L A M A L G L V V P M L H H L C G W
 2521 GACCTCTGGTACTGCTTCCACCTGTGGCTGGCTGGCTGCCCCACCGAGGGCAGGGCGG 2580
 D L W Y C F H L C L A W L P H R G Q R R
 2581 GGCGCAGACGCCCTGTCTATGATGCCCTTGGTGTCTTTGACAAAGCTCAGAGTGTGTG 2640
 G A D A L F Y D A F V V F D K A Q S A V
 2641 GCGACTGGGTGTACACAGAGCTGGGGGTGCAGCTGGAGAGCGCCGTGGGGGCGCGCA 2700
 A D W V Y N E L R V Q L E E R R G R R A
 2701 CTGGGCTGTGGCTGGAGGAGGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACTG 2760
 L R L C L E E R D W L P G K T L F E N L
 2761 TGGGCTCAGTCTACAGCAGCGCAGACCCCTGTTGTGCTGGCCACACCGAACGGTGT 2820
 W A S V Y S S R K T L F V L A H T D R V
 2821 AGCGGCTCTTGGTGGCAGTTTCTGCTGGCCAGCAGCGCTGCTGGAGGACCGCAAG 2880
 S G L L R A S F L L A Q Q R L L E D R K
 2881 GACGTTGTAGTGTGGTGTCTGGGCTGGATGCTACCGCTCCCGTACGTGGGCTG 2940
 D V V V L V I L R P D A Y R S R Y V R L
 2941 CGCCAGCGGCTCTGGCGCAGAGTGTCTCTCTGGCCCCACCAGCCCGTGGGCAGGGC 3000
 R Q R L C R Q S V L L W P H Q P R G Q G
 3001 AGCTTCTGGGCCAGCTGGGCACAGCCCTGACCAGGGACAACCGCACTTCTATAACCG 3060
 S F W A Q L G T A L T R D N R H F Y N R
 3061 AACTTCTGCGGGGCCCCACGACAGCCGAATAG 3093 (SEQ ID NO:1 2395-3147)
 N F C R G P T T A E * (SEQ ID NO:2 781-1030)

Amended

FIG. 6

SWINE	1	MCPRCT--LHPLSLVQVITALAATLAQGRIPAFILPCELOPHGLVNCWMLFKSVPHFSAA	58	SWINE
HUMAN	1	MG-CRSALHPLSLVQVIMLMTIALGTLPAFILPCELOPHGLVNCWMLFKSVPHFSMA	59	HUMAN
MOUSE	1	MLRPRT-LHPLSLVQVAVIAETIALGTLPAFILPCELOPHGLVNCWMLFKSVPRFSAA	59	MOUSE
CAT	1	MGP-CHGALHPLSLVQAAALAVALAQGTLPFILPCELOPHGLVNCWMLFKSVPHFSAA	59	CAT
* ***** . ** . ** . ***** . . **** . * . ***** . ** *				
SWINE	59	APRANVTSLSLSNRIHHLHDSDFVHLSLRLTNLKNWCPPAGLSMFEPCMTIEPNTF	118	SWINE
HUMAN	60	APRGWTSLSLSNRIHHLHDSDFAHLPSPRLHNLKNWCPPVGLSPMFEPCMTIEPSTF	119	HUMAN
MOUSE	60	ASCNITRLSLISNRIHHLHDSDFVHLSNLRLNLKNWCPPTGLSPLHFSCHMTIEPRTF	119	MOUSE
CAT	60	APRGWTSLSLSNRIHHLHDSDFVHLSLRLNLKNWCPPASLSMFEPCMTIEPHTF	119	CAT
* . . * . * ** ***** . ** . ** . * ** ***** . *** . ** . ***** . ** *				
SWINE	119	LAVPTLEEINLSYNSITTVPALPDSLVLSLSRNTNIVLDPHTLTGLHALRYLYMDGNCY	178	SWINE
HUMAN	120	LAVPTLEEINLSYNNIMVPAKSLISLSLSHTNIMLDSASLAGLHALRFTFMDGNCY	179	HUMAN
MOUSE	120	LAMPTLEEINLSYNGITTVPRLPSSLWNLSLSHNTNIMLDANSAGLYSLRFLMDGNCY	179	MOUSE
CAT	120	LAVPTLEEINLSYNSITTVPALPSSLVLSLSRNTNIVLDPANLAGLSLRFITFDGNCY	179	CAT
** . . ***** . *** . ** . ** . ***** . ** * . ** . ** . *****				
SWINE	179	YKNPCQALEWPGALLGLNLTHLSLKYNNLTVPRLSPSLETLLSYNHIIVTLTPED	238	SWINE
HUMAN	180	YKNPCQALEWPGALLGLNLTHLSLKYNNLTWPRNLPSSLEYLLSYNRIIVKLAPE	239	HUMAN
MOUSE	180	YKNPCTGAVKVPAGALLGLNLTHLSLKYNNLTWPRQLPPSLEYLLSYNLIVKLAPE	239	MOUSE
CAT	180	YKNPCQALQVAPGALLGLNLTHLSLKYNNLTAVPRGLPPSLEYLLSYNHIITLAPED	239	CAT
***** * . * ***** . ***** . ** * . ** . ** . *** * . * ** *				
SWINE	239	LANLTAIRVLVDGNGCRCDHARNPCRECPKDHKLSHSDTFSHLSRLIEGLVMDSSLYNL	298	
			Amended	(SEQ ID NO:2 1-298)
HUMAN	240	LANLTAIRVLVDGNGCRCDHARNPCMECPRHFPOLHPDTFSHLSRLIEGLVMDSSLYNL	299	
				(SEQ ID NO:4 1-299)
MOUSE	240	LANLTSRLVLVDGNGCRCDHARNPCIECGKSLHHPETPHLSRLIEGLVMDSSLYNL	299	
				(SEQ ID NO:6 1-299)
CAT	240	LANLTAIRVLVDGNGCRCDHARNPCMECPKGFPHLPDTFSHLNIEGLVMDSSLYNL	299	
			***** . ***** . ***** . ** * . . ** . ** . ** . ***** . *	(SEQ ID NO:8 1-299)

FIG. 7

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SWINE 299 DARWFRGLDRQLVLDLSENFLYDCITKTTFAPQGLTLRKINLSFNYHKVVSFAHLHLAPS 358
HUMAN 300 NASWFRGLGLNLRLVLDLSENFLYKCIITKTFAQGLTLRKINLSFNYQKRVVSFAHLHLAPS 359
MOUSE 300 NSSWFRGLGLNLVLDLSENFLYKSIHININAFQNLIRLRKINLSFNYKRVVSFAHLHLASS 359
CAT 300 NPSWFRHALGNLWLDLSENFLYDCITKTTFAPQGLTLRRINLSFNYHKVVSFAHLHLAPS 359
      * * * * *
SWINE 359 FGHIRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMFNFNQALSIFGAFFGLLY 418
HUMAN 360 FGSLVAKELDMHGIFFRSLDEITLRLPLRLPMLQTLRLQMFNFNQALGIFRAFFGLRY 419
MOUSE 360 FKNLVSLQELINNGIFFRSLNKYTLRWLADLPKLHLHLQMFNFNQALSIFGTFRALRF 419
CAT 360 FGSLLSQLQDMHGIFFRSLSETTLRSVLHPLMLQSLHLQMFNFNQALSIFGAFFGLRY 419
      * * * * *
SWINE 419 VDLSDNRISGAARPVAITREVDGR-ERWVLPNRNLAPRPLDTLRSEDFMENCKAFSFTILD 477
HUMAN 420 VDLSDNRISGAELTAIMGADGG-EKWVLPQGLAPAPVDPSPSEDFRNCSTLNFTILD 478
MOUSE 420 VDLSDNRISGSPSTLSEATPEEADAEQEELSDADHPAPLGTPTASKNFMDRCKNFKFTMD 479
CAT 420 VDLSDNRISGAMELAAATGEVDGG-ERVRIPSGDLALGPPGTPSSEGFPGCKTLNFTILD 478
      *****
SWINE 478 LSRNINLVTIQSEMFARLSRLECLRLSHNSISQAVNGSGFVPLTSLRWLDLSHNKLDLYHG 537
HUMAN 479 LSRNINLVTIQSEMFAQLSHLQCLRLSHNCISQAVNGSGFPLTGLQVLDLSRNKLDLYHE 538
MOUSE 480 LSRNINLVTIKPEMFVNLSRLQCLLSHNSIAQAVNGSGFPLTINLQVLDLSHNKLDLYHW 539
CAT 479 LSRNINLVTIQSEMFARLSRQCLLSRNSISQAVNGSGFPLTSLQVLDLSHNKLDLYHG 538
      *****

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FIG. 8

SWINE	538	RSFTETLPRIEALDLSYNSQPFIMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA	597
HUMAN	539	HSFTETLPRIEALDLSYNSQPFQGVGHNLSFVAHLRTLRHLSLAHNIHSQVSQQLCST	598
MOUSE	540	KSFSELPQLQALDLSYNSQPFSSIKGIGHNLSFVAHLSMLHLSLAHNDIHRVSSHNSN	599
CAT	539	RSFTETLPRIEALDLSYNSQPFIMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA	598
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * *			
SWINE	598	SLCALDFSGNDLSRMWAEGLDLYLHFFQGLPSLWDLDSQNLHLTLPRALDNLPKSLKHL	657
HUMAN	599	SLRALDFSGVALGHMWAEGLDLYLHFFQGLSGLIWLDSQNLHLTLPQTILNLPKSLQVL	658
MOUSE	600	SVRFIDFSQNGRMWDEGGLYLHFFQGLSGLIKLDSQNLHLRPNLNLPKSLKLL	659
CAT	599	SLRALDFSGNALSRWAEGLDLYLHFFQGLPSLWDLDSQNLHLTLPRITLNLPKSLRL	658
* * * * * * * * * * * * * * * * * * * * * * * * * * * * *			
SWINE	658	HLRDNNAFFNWSLTLIPKLETLDLAGNQLKALNGSLPAGTQLPRIDLDSGNSIGFVNP	717
HUMAN	659	RLRDNNAFFNWSLTLIPKLEVLDLAGNRLKALNGSLPAGTQLRLRLDVSQNSISFVAP	718
MOUSE	660	SLRDNLSFFNWSLTLIPNLEVLDLAGNQLKALNGTLPNGTLLQKLDVSSNSIVSWP	719
CAT	659	RLRDNNAFFNWSLTLIPRIEALDLAGNQLKALNGSLPAGTQLRLDLSSNSISFVAS	718
* * * * * * * * * * * * * * * * * * * * * * * * * * * * *			
SWINE	718	GFFALAKQEEINLSANALKTIVEPSWFGSMGILKVLDSANPLHCACGAFTVGFLEVQ	777
HUMAN	719	GFFSKAKELREINLSANALKTVDSWFGPLASALQILDVSANPLHCACGAFTDFLEVQ	778
MOUSE	720	AFFALAVELKEVNLSHNLIKTVDRSWFGPIVNNITVLDVRSNPLHCACGAFTVLLLEVQ	779
CAT	719	SFFALATRLREINLSANALKTIVEPSWFGSLAGTLKVLDTGNPLHCACGAFTVDFLEVQ	778
* * * * * * * * * * * * * * * * * * * * * * * * * * * * *			
SWINE	778	AAVPGCLPSRVKCGSPGQLQGRSIFAQDLRLCLDETLQWCFGLSLIAVALGIVPMLHHL	837
		Amended	(SEQ ID NO:2 538-837)
HUMAN	779	AAVPGCLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSDCFGLSLIAVALGIVPMLHHL	838
			(SEQ ID NO:4 539-838)
MOUSE	780	TKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWCFGLSLIAVAVGMVPIHHL	839
			(SEQ ID NO:6 540-839)
CAT	779	AAVPGCLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSDCFGLSLITVALGLAVPMLHHL	838
* * * * * * * * * * * * * * * * * * * * * * * * * * * * *			
			(SEQ ID NO:8 539-838)

FIG. 9

SWINE	838	CGNDLWYCFHLCIAWLPFRGQRRGAD--ALFYDAFWFDKAQSAVADWYNEIRVQLEER	895
HUMAN	839	CGNDLWYCFHLCIAWLPFRGQSGRDEDALPYDAFWFDKQSAVADWYNEIRGQLEEC	898
MOUSE	840	CGNDVWYCFHLCIAWLPLIARSRRSACA-LPYDAFWFDKAQSAVADWYNEIRVRLEGR	898
CAT	839	CGNDLWYCFHLCIAWLPRGRFRGAD--ALPYDAFWFDKAQSAVADWYNEIRVLEER	896
, **,, *, *****, *****, **,			
SWINE	896	RGRPALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHIDRVSGLLRASFLLAQRL	955
HUMAN	899	RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHIDRVSGLLRASFLLAQRL	958
MOUSE	899	RGRPALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHIDRVSGLLRTSFLLAQRL	958
CAT	897	RGRPALRLCLEERDWLPGKTLFENLWASVYSSKMLFVLAHIDRVSGLLRASFLLAQRL	956
, ***, *****, *****, *, ***, *****, *****, *****,			
SWINE	956	LEDKDWVWLILRPDAYRSRYVRLRQLCRQSVLLWPHQPGQGSFWAQLGTALTRDN	1015
HUMAN	959	LEDKDWVWLILSPDGRSRVRLRQLCRQSVLLWPHQPGQGSFWAQLGVALTRDNH	1018
MOUSE	959	LEDKDWVWLILRPDAHRSRYVRLRQLCRQSVLWPHQPGQGSFWAQLGTALTRDN	1018
CAT	957	LEDKDWVWLILRPDAHRSRYVRLRQLCRQSVLLWPHQPGQGSFWAQLGTALTRDNQ	1016
*****, **, ***** *****, ***, ***, *****, *****			
SWINE	1016	HEYNRNFCRPTTAE (SEQ ID NO:2 838-1030)	1030
HUMAN	1019	HEYNRNFCQQTAE (SEQ ID NO:4 839-1032)	1032
MOUSE	1019	HEYNRNFCRQTAE (SEQ ID NO:6 840-1032)	1032
CAT	1017	HEYNRNFCRPTTAE (SEQ ID NO:8 839-1031)	1031
****, ***, ***, ***,			